



## SEQUENCE LISTING

<110> KAKIMOTO, TATSUO  
HIGUCHI, MASAYUKI  
INOUE, TSUTOMU

<120> ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY  
TO CYTOKININ RECEPTOR

<130> Q65478

<140> 09/918,508

<141> 2001-08-01

<150> JP 2001-073812

<151> 2001-03-15

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 3531

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(3531)

<400> 1

atg tct ata act tgt gag ctc ttg aat ctt act tca aag aaa gct aag	48
Met Ser Ile Thr Cys Glu Leu Leu Asn Leu Thr Ser Lys Lys Ala Lys	
1 5 10 15	
aag tcg tcg agc agt gac aag aaa tgg cta aag aag cct ctc ttc ttc	96
Lys Ser Ser Ser Ser Asp Lys Lys Trp Leu Lys Lys Pro Leu Phe Phe	
20 25 30	
ctg att ttg tgt ggc tct ttg gta att gtt ttg gtt atg ttc tta cgg	144
Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg	
35 40 45	
tta ggt aga agt cag aag gag gag aca gat tct tgt aat gga gaa gag	192
Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu	
50 55 60	
aaa gtg ttg tat aga cat caa aat gtc aca aga agt gag att cat gat	240
Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp	
65 70 75 80	
ttg gtc tct ttg ttc tct gat tca gat cag gta aca tcc ttt gaa tgt	288
Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys	
85 90 95	
cat aag gaa tca agc cct gga atg tgg aca aac tat ggt att aca tgt	336
His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys	
100 105 110	

tcc ctg agt gtg cgt tct gat aaa caa gag act aga ggg ctt ccc tgg	384
Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp	
115 120 125	
aat ctt ggc tta gga cat tct atc tca tca aca tct tgt atg tgt ggt	432
Asn Leu Gly Leu Gly His Ser Ile Ser Ser Thr Ser Cys Met Cys Gly	
130 135 140	
aat ctt gaa ccg att tta cag caa cct gaa aac ctt gag gaa gaa aac	480
Asn Leu Glu Pro Ile Leu Gln Gln Pro Glu Asn Leu Glu Glu Glu Asn	
145 150 155 160	
cat gaa gaa ggg ctg gag cag ggt ttg tca tcg tat tta aga aat gca	528
His Glu Glu Gly Leu Glu Gln Gly Leu Ser Ser Tyr Leu Arg Asn Ala	
165 170 175	
tgg tgg tgt cta atc ctt ggt gtg tta gtg tgc cat aag att tat gta	576
Trp Trp Cys Leu Ile Leu Gly Val Leu Val Cys His Lys Ile Tyr Val	
180 185 190	
tct cat tct aaa gca cga ggt gag agg aaa gag aaa gta cat ctg caa	624
Ser His Ser Lys Ala Arg Gly Glu Arg Lys Glu Lys Val His Leu Gln	
195 200 205	
gag gct tta gct cca aag aag cag caa caa cgt gct cag act tct tct	672
Glu Ala Leu Ala Pro Lys Lys Gln Gln Gln Arg Ala Gln Thr Ser Ser	
210 215 220	
aga ggg gct gga aga tgg agg aag aat atc ctt ctc ctt ggt att tta	720
Arg Gly Ala Gly Arg Trp Arg Lys Asn Ile Leu Leu Leu Gly Ile Leu	
225 230 235 240	
gga gga gtt tcc ttc tct gtt tgg tgg ttt tgg gac act aat gag gag	768
Gly Gly Val Ser Phe Ser Val Trp Trp Phe Trp Asp Thr Asn Glu Glu	
245 250 255	
atc ata atg aaa agg agg gag act ttg gca aac atg tgt gac gaa cga	816
Ile Ile Met Lys Arg Arg Glu Thr Leu Ala Asn Met Cys Asp Glu Arg	
260 265 270	
gca cgt gtt tta caa gat cag ttc aat gtt agc ttg aac cat gtt cat	864
Ala Arg Val Leu Gln Asp Gln Phe Asn Val Ser Leu Asn His Val His	
275 280 285	
gcc ttg tct att ctt gta tct aca ttt cat cat ggt aaa atc cca tct	912
Ala Leu Ser Ile Leu Val Ser Thr Phe His His Gly Lys Ile Pro Ser	
290 295 300	
gcc att gat cag aga aca ttt gaa gaa tat act gag aga aca aac ttt	960
Ala Ile Asp Gln Arg Thr Phe Glu Glu Tyr Thr Glu Arg Thr Asn Phe	
305 310 315 320	
gag agg cca ctt act agt ggt gta gcg tat gct ttg aaa gtc cca cac	1008
Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala Leu Lys Val Pro His	
325 330 335	

tca gaa aga gag aaa ttt gaa aag gag cat gga tgg gca ata aag aaa	1056
Ser Glu Arg Glu Lys Phe Glu Lys Glu His Gly Trp Ala Ile Lys Lys	
340 345 350	
atg gaa act gag gac cag aca gtt gta caa gat tgt gtt cct gaa aac	1104
Met Glu Thr Glu Asp Gln Thr Val Val Gln Asp Cys Val Pro Glu Asn	
355 360 365	
ttt gat ccc gca ccg att caa gac gaa tac gcg cca gtt ata ttt gct	1152
Phe Asp Pro Ala Pro Ile Gln Asp Glu Tyr Ala Pro Val Ile Phe Ala	
370 375 380	
caa gaa act gtt tcc cat att gta tcg gtc gac atg atg tct gga gaa	1200
Gln Glu Thr Val Ser His Ile Val Ser Val Asp Met Met Ser Gly Glu	
385 390 395 400	
gaa gac cgt gaa aac atc tta cgg gca agg gca tca gga aaa gga gtg	1248
Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Ala Ser Gly Lys Gly Val	
405 410 415	
tta aca tct cca ttt aag ctt ctt aag tca aat cat ctt ggt gtt gtg	1296
Leu Thr Ser Pro Phe Lys Leu Leu Lys Ser Asn His Leu Gly Val Val	
420 425 430	
ttg acc ttt gct gtc tat gac acg agc cta ccg cct gat gct aca gaa	1344
Leu Thr Phe Ala Val Tyr Asp Thr Ser Leu Pro Pro Asp Ala Thr Glu	
435 440 445	
gaa cag cgt gtt gaa gca act att ggg tac ctt ggt gca tca tat gat	1392
Glu Gln Arg Val Glu Ala Thr Ile Gly Tyr Leu Gly Ala Ser Tyr Asp	
450 455 460	
atg cca tcg ctg gtg gag aaa ctt ctt cac caa ctt gcc agc aaa cag	1440
Met Pro Ser Leu Val Glu Lys Leu Leu His Gln Leu Ala Ser Lys Gln	
465 470 475 480	
aca att gct gtg gat gtt tac gac aca act aac act tca ggt cta ata	1488
Thr Ile Ala Val Asp Val Tyr Asp Thr Thr Asn Thr Ser Gly Leu Ile	
485 490 495	
aaa atg tat ggc tca gaa att ggg gat ata agt gag cag cat ata agt	1536
Lys Met Tyr Gly Ser Glu Ile Gly Asp Ile Ser Glu Gln His Ile Ser	
500 505 510	
agc ctt gat ttt ggt gat cca tca agg aac cat gag atg cat tgc agg	1584
Ser Leu Asp Phe Gly Asp Pro Ser Arg Asn His Glu Met His Cys Arg	
515 520 525	
ttt aag cat aaa ctt ccc att ccc tgg aca gcg ata aca ccg tcg atc	1632
Phe Lys His Lys Leu Pro Ile Pro Trp Thr Ala Ile Thr Pro Ser Ile	
530 535 540	
tta gtt ctg gtt att act ttt ctt gtt ggt tat att tta tat gaa gcc	1680
Leu Val Leu Val Ile Thr Phe Leu Val Gly Tyr Ile Leu Tyr Glu Ala	
545 550 555 560	

atc aac cga att gcg aca gtt gaa gag gat tgt cag aag atg agg gaa	1728
Ile Asn Arg Ile Ala Thr Val Glu Glu Asp Cys Gln Lys Met Arg Glu	
565 570 575	
ctc aaa gct cgt gct gag gcc gct gac att gca aag tca cag ttc cta	1776
Leu Lys Ala Arg Ala Glu Ala Ala Asp Ile Ala Lys Ser Gln Phe Leu	
580 585 590	
gca act gtt tct cat gag ata cgg act ccg atg aat gga gtt tta gga	1824
Ala Thr Val Ser His Glu Ile Arg Thr Pro Met Asn Gly Val Leu Gly	
595 600 605	
atg ctg aaa atg ctg atg gac acc gat ctt gat gcg aag cag atg gac	1872
Met Leu Lys Met Leu Met Asp Thr Asp Leu Asp Ala Lys Gln Met Asp	
610 615 620	
tat gcg caa act gct cat ggc agt ggg aag gat ctt aca tca cta ata	1920
Tyr Ala Gln Thr Ala His Gly Ser Gly Lys Asp Leu Thr Ser Leu Ile	
625 630 635 640	
aat gag gtt ctt gat cag gca aag att gaa tcc gga agg ctc gag ctt	1968
Asn Glu Val Leu Asp Gln Ala Lys Ile Glu Ser Gly Arg Leu Glu Leu	
645 650 655	
gaa aat gtg cct ttt gat atg cgt ttt att ctt gat aat gtt tca tct	2016
Glu Asn Val Pro Phe Asp Met Arg Phe Ile Leu Asp Asn Val Ser Ser	
660 665 670	
ctc ctc tct ggc aag gca aat gaa aaa gga att gag ttg gcc gtt tat	2064
Leu Leu Ser Gly Lys Ala Asn Glu Lys Gly Ile Glu Leu Ala Val Tyr	
675 680 685	
gtt tct agt caa gtt cct gat gtt gta gtc ggt gat ccg agt cgg ttc	2112
Val Ser Ser Gln Val Pro Asp Val Val Val Gly Asp Pro Ser Arg Phe	
690 695 700	
cgg cag atc att aca aac ctg gtt gga aac tca atc aaa ttc aca cag	2160
Arg Gln Ile Ile Thr Asn Leu Val Gly Asn Ser Ile Lys Phe Thr Gln	
705 710 715 720	
gaa agg gga cac ata ttt atc tca gtg cac ctt gca gat gag gta aag	2208
Glu Arg Gly His Ile Phe Ile Ser Val His Leu Ala Asp Glu Val Lys	
725 730 735	
gag cct ctt act att gaa gac gca gtg cta aaa cag cga cta gct tta	2256
Glu Pro Leu Thr Ile Glu Asp Ala Val Leu Lys Gln Arg Leu Ala Leu	
740 745 750	
gga tgc agc gag tcc ggt gag aca gtt agc ggg ttt cct gcg gta aat	2304
Gly Cys Ser Glu Ser Gly Glu Thr Val Ser Gly Phe Pro Ala Val Asn	
755 760 765	
gca tgg gga agc tgg aag aat ttc aag aca tgt tac agt act gag agt	2352
Ala Trp Gly Ser Trp Lys Asn Phe Lys Thr Cys Tyr Ser Thr Glu Ser	
770 775 780	

cag aat tct gat caa atc aaa ttg cta gtt aca gtg gag gac act gga Gln Asn Ser Asp Gln Ile Lys Leu Leu Val Thr Val Glu Asp Thr Gly 785 790 795 800	2400
gtt ggc ata cct gtg gat gca caa ggc cga atc ttc aca cct ttt atg Val Gly Ile Pro Val Asp Ala Gln Gly Arg Ile Phe Thr Pro Phe Met 805 810 815	2448
caa gcc gac agt tcc aca tcg cgg act tat ggt gga act ggc ata ggt Gln Ala Asp Ser Ser Thr Ser Arg Thr Tyr Gly Gly Thr Gly Ile Gly 820 825 830	2496
ttg agt ata agc aaa cgt ttg gtt gaa ctc atg caa gga gag atg ggg Leu Ser Ile Ser Lys Arg Leu Val Glu Leu Met Gln Gly Glu Met Gly 835 840 845	2544
ttt gtg agt gag ccc ggg ata ggc agt act ttt tca ttt act gga gtt Phe Val Ser Glu Pro Gly Ile Gly Ser Thr Phe Ser Phe Thr Gly Val 850 855 860	2592
ttc ggg aaa gca gaa aca aat acg tcg att act aag ctg gaa cga ttc Phe Gly Lys Ala Glu Thr Asn Thr Ser Ile Thr Lys Leu Glu Arg Phe 865 870 875 880	2640
gat cta gct att cag gag ttt aca gga ttg aga gca tta gtt att gat Asp Leu Ala Ile Gln Glu Phe Thr Gly Leu Arg Ala Leu Val Ile Asp 885 890 895	2688
aac aga aac att aga gca gag gtc acc agg tac gaa ctt cgg aga ctg Asn Arg Asn Ile Arg Ala Glu Val Thr Arg Tyr Glu Leu Arg Arg Leu 900 905 910	2736
gga ata tct gca gac att gtt tca agt ctg aga atg gca tgc act tgt Gly Ile Ser Ala Asp Ile Val Ser Ser Leu Arg Met Ala Cys Thr Cys 915 920 925	2784
tgt atc agc aaa tta gaa aat ttg gct atg att cta ata gac aaa gac Cys Ile Ser Lys Leu Glu Asn Leu Ala Met Ile Leu Ile Asp Lys Asp 930 935 940	2832
gcc tgg aac aag gaa gaa ttt tca gta ctt gac gag ttg ttt acc cga Ala Trp Asn Lys Glu Glu Phe Ser Val Leu Asp Glu Leu Phe Thr Arg 945 950 955 960	2880
agc aaa gta acc ttt aca aga gtc cca aag att ttt ctt ttg gca act Ser Lys Val Thr Phe Thr Arg Val Pro Lys Ile Phe Leu Leu Ala Thr 965 970 975	2928
tct gca act ctt act gag cgc agt gag atg aag tct act ggt ctc atc Ser Ala Thr Leu Thr Glu Arg Ser Glu Met Lys Ser Thr Gly Leu Ile 980 985 990	2976
gat gag gtg gtg ata aag cct ctt cgg atg agt gtc tta ata tgt tgc Asp Glu Val Val Ile Lys Pro Leu Arg Met Ser Val Leu Ile Cys Cys 995 1000 1005	3024

ttg caa gaa acc ctt gtc aat ggc aag aag agg caa ccg aac aga cag	3072
Leu Gln Glu Thr Leu Val Asn Gly Lys Lys Arg Gln Pro Asn Arg Gln	
1010 1015 1020	
cga aga aat ctt gga cac ttg cta aga gaa aaa cag att ctg gtt gtg	3120
Arg Arg Asn Leu Gly His Leu Leu Arg Glu Lys Gln Ile Leu Val Val	
1025 1030 1035 1040	
gat gat aat ctt gtg aac aga cga gtt gca gaa ggt gca ctt aag aaa	3168
Asp Asp Asn Leu Val Asn Arg Arg Val Ala Glu Gly Ala Leu Lys Lys	
1045 1050 1055	
tat gga gct att gtt aca tgc gtt gag agt ggc aaa gct gca ttg gca	3216
Tyr Gly Ala Ile Val Thr Cys Val Glu Ser Gly Lys Ala Ala Leu Ala	
1060 1065 1070	
atg ctt aag ccg cct cat aac ttc gat gct tgc ttc atg gat ctc cag	3264
Met Leu Lys Pro Pro His Asn Phe Asp Ala Cys Phe Met Asp Leu Gln	
1075 1080 1085	
atg cct gaa atg gat gga ttt gaa gcg aca agg aga gtc cgt gag ctg	3312
Met Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Val Arg Glu Leu	
1090 1095 1100	
gag agg gaa atc aat aag aaa ata gct tct gga gaa gtt tca gct gaa	3360
Glu Arg Glu Ile Asn Lys Lys Ile Ala Ser Gly Glu Val Ser Ala Glu	
1105 1110 1115 1120	
atg ttc tgt aaa ttt agt agt tgg cac gtc ccg ata tta gca atg aca	3408
Met Phe Cys Lys Phe Ser Ser Trp His Val Pro Ile Leu Ala Met Thr	
1125 1130 1135	
gca gat gtt att cag gct act cat gaa gaa tgc atg aaa tgt gga atg	3456
Ala Asp Val Ile Gln Ala Thr His Glu Glu Cys Met Lys Cys Gly Met	
1140 1145 1150	
gat ggt tat gta tca aaa ccg ttt gaa gag gaa gtg ctc tac aca gcg	3504
Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Val Leu Tyr Thr Ala	
1155 1160 1165	
gta gca aga ttc ttt gaa cct tgt taa	3531
Val Ala Arg Phe Phe Glu Pro Cys	
1170 1175	
<210> 2	
<211> 1176	
<212> PRT	
<213> Arabidopsis thaliana	
<400> 2	
Met Ser Ile Thr Cys Glu Leu Leu Asn Leu Thr Ser Lys Lys Ala Lys	
1 5 10 15	
Lys Ser Ser Ser Ser Asp Lys Lys Trp Leu Lys Lys Pro Leu Phe Phe	
20 25 30	

Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg  
 35 40 45  
 Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu  
 50 55 60  
 Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp  
 65 70 75 80  
 Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys  
 85 90 95  
 His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys  
 100 105 110  
 Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp  
 115 120 125  
 Asn Leu Gly Leu Gly His Ser Ile Ser Ser Thr Ser Cys Met Cys Gly  
 130 135 140  
 Asn Leu Glu Pro Ile Leu Gln Gln Pro Glu Asn Leu Glu Glu Glu Asn  
 145 150 155 160  
 His Glu Glu Gly Leu Glu Gln Gly Leu Ser Ser Tyr Leu Arg Asn Ala  
 165 170 175  
 Trp Trp Cys Leu Ile Leu Gly Val Leu Val Cys His Lys Ile Tyr Val  
 180 185 190  
 Ser His Ser Lys Ala Arg Gly Glu Arg Lys Glu Lys Val His Leu Gln  
 195 200 205  
 Glu Ala Leu Ala Pro Lys Lys Gln Gln Gln Arg Ala Gln Thr Ser Ser  
 210 215 220  
 Arg Gly Ala Gly Arg Trp Arg Lys Asn Ile Leu Leu Leu Gly Ile Leu  
 225 230 235 240  
 Gly Gly Val Ser Phe Ser Val Trp Trp Phe Trp Asp Thr Asn Glu Glu  
 245 250 255  
 Ile Ile Met Lys Arg Arg Glu Thr Leu Ala Asn Met Cys Asp Glu Arg  
 260 265 270  
 Ala Arg Val Leu Gln Asp Gln Phe Asn Val Ser Leu Asn His Val His  
 275 280 285  
 Ala Leu Ser Ile Leu Val Ser Thr Phe His His Gly Lys Ile Pro Ser  
 290 295 300  
 Ala Ile Asp Gln Arg Thr Phe Glu Glu Tyr Thr Glu Arg Thr Asn Phe  
 305 310 315 320  
 Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala Leu Lys Val Pro His  
 325 330 335

Ser Glu Arg Glu Lys Phe Glu Lys Glu His Gly Trp Ala Ile Lys Lys  
 340 345 350  
 Met Glu Thr Glu Asp Gln Thr Val Val Gln Asp Cys Val Pro Glu Asn  
 355 360 365  
 Phe Asp Pro Ala Pro Ile Gln Asp Glu Tyr Ala Pro Val Ile Phe Ala  
 370 375 380  
 Gln Glu Thr Val Ser His Ile Val Ser Val Asp Met Met Ser Gly Glu  
 385 390 395 400  
 Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Ala Ser Gly Lys Gly Val  
 405 410 415  
 Leu Thr Ser Pro Phe Lys Leu Leu Lys Ser Asn His Leu Gly Val Val  
 420 425 430  
 Leu Thr Phe Ala Val Tyr Asp Thr Ser Leu Pro Pro Asp Ala Thr Glu  
 435 440 445  
 Glu Gln Arg Val Glu Ala Thr Ile Gly Tyr Leu Gly Ala Ser Tyr Asp  
 450 455 460  
 Met Pro Ser Leu Val Glu Lys Leu Leu His Gln Leu Ala Ser Lys Gln  
 465 470 475 480  
 Thr Ile Ala Val Asp Val Tyr Asp Thr Thr Asn Thr Ser Gly Leu Ile  
 485 490 495  
 Lys Met Tyr Gly Ser Glu Ile Gly Asp Ile Ser Glu Gln His Ile Ser  
 500 505 510  
 Ser Leu Asp Phe Gly Asp Pro Ser Arg Asn His Glu Met His Cys Arg  
 515 520 525  
 Phe Lys His Lys Leu Pro Ile Pro Trp Thr Ala Ile Thr Pro Ser Ile  
 530 535 540  
 Leu Val Leu Val Ile Thr Phe Leu Val Gly Tyr Ile Leu Tyr Glu Ala  
 545 550 555 560  
 Ile Asn Arg Ile Ala Thr Val Glu Glu Asp Cys Gln Lys Met Arg Glu  
 565 570 575  
 Leu Lys Ala Arg Ala Glu Ala Ala Asp Ile Ala Lys Ser Gln Phe Leu  
 580 585 590  
 Ala Thr Val Ser His Glu Ile Arg Thr Pro Met Asn Gly Val Leu Gly  
 595 600 605  
 Met Leu Lys Met Leu Met Asp Thr Asp Leu Asp Ala Lys Gln Met Asp  
 610 615 620  
 Tyr Ala Gln Thr Ala His Gly Ser Gly Lys Asp Leu Thr Ser Leu Ile  
 625 630 635 640



Asn Glu Val Leu Asp Gln Ala Lys Ile Glu Ser Gly Arg Leu Glu Leu  
                                 645                                650                                655  
 Glu Asn Val Pro Phe Asp Met Arg Phe Ile Leu Asp Asn Val Ser Ser  
                                 660                                665                                670  
 Leu Leu Ser Gly Lys Ala Asn Glu Lys Gly Ile Glu Leu Ala Val Tyr  
                                 675                                680                                685  
 Val Ser Ser Gln Val Pro Asp Val Val Val Gly Asp Pro Ser Arg Phe  
                                 690                                695                                700  
 Arg Gln Ile Ile Thr Asn Leu Val Gly Asn Ser Ile Lys Phe Thr Gln  
 705                                710                                715                                720  
 Glu Arg Gly His Ile Phe Ile Ser Val His Leu Ala Asp Glu Val Lys  
                                 725                                730                                735  
 Glu Pro Leu Thr Ile Glu Asp Ala Val Leu Lys Gln Arg Leu Ala Leu  
                                 740                                745                                750  
 Gly Cys Ser Glu Ser Gly Glu Thr Val Ser Gly Phe Pro Ala Val Asn  
                                 755                                760                                765  
 Ala Trp Gly Ser Trp Lys Asn Phe Lys Thr Cys Tyr Ser Thr Glu Ser  
                                 770                                775                                780  
 Gln Asn Ser Asp Gln Ile Lys Leu Leu Val Thr Val Glu Asp Thr Gly  
 785                                790                                795                                800  
 Val Gly Ile Pro Val Asp Ala Gln Gly Arg Ile Phe Thr Pro Phe Met  
                                 805                                810                                815  
 Gln Ala Asp Ser Ser Thr Ser Arg Thr Tyr Gly Gly Thr Gly Ile Gly  
                                 820                                825                                830  
 Leu Ser Ile Ser Lys Arg Leu Val Glu Leu Met Gln Gly Glu Met Gly  
                                 835                                840                                845  
 Phe Val Ser Glu Pro Gly Ile Gly Ser Thr Phe Ser Phe Thr Gly Val  
                                 850                                855                                860  
 Phe Gly Lys Ala Glu Thr Asn Thr Ser Ile Thr Lys Leu Glu Arg Phe  
 865                                870                                875                                880  
 Asp Leu Ala Ile Gln Glu Phe Thr Gly Leu Arg Ala Leu Val Ile Asp  
                                 885                                890                                895  
 Asn Arg Asn Ile Arg Ala Glu Val Thr Arg Tyr Glu Leu Arg Arg Leu  
                                 900                                905                                910  
 Gly Ile Ser Ala Asp Ile Val Ser Ser Leu Arg Met Ala Cys Thr Cys  
                                 915                                920                                925  
 Cys Ile Ser Lys Leu Glu Asn Leu Ala Met Ile Leu Ile Asp Lys Asp  
                                 930                                935                                940

Ala Trp Asn Lys Glu Glu Phe Ser Val Leu Asp Glu Leu Phe Thr Arg  
 945 950 955 960  
 Ser Lys Val Thr Phe Thr Arg Val Pro Lys Ile Phe Leu Leu Ala Thr  
 965 970 975  
 Ser Ala Thr Leu Thr Glu Arg Ser Glu Met Lys Ser Thr Gly Leu Ile  
 980 985 990  
 Asp Glu Val Val Ile Lys Pro Leu Arg Met Ser Val Leu Ile Cys Cys  
 995 1000 1005  
 Leu Gln Glu Thr Leu Val Asn Gly Lys Lys Arg Gln Pro Asn Arg Gln  
 1010 1015 1020  
 Arg Arg Asn Leu Gly His Leu Leu Arg Glu Lys Gln Ile Leu Val Val  
 1025 1030 1035 1040  
 Asp Asp Asn Leu Val Asn Arg Arg Val Ala Glu Gly Ala Leu Lys Lys  
 1045 1050 1055  
 Tyr Gly Ala Ile Val Thr Cys Val Glu Ser Gly Lys Ala Ala Leu Ala  
 1060 1065 1070  
 Met Leu Lys Pro Pro His Asn Phe Asp Ala Cys Phe Met Asp Leu Gln  
 1075 1080 1085  
 Met Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Val Arg Glu Leu  
 1090 1095 1100  
 Glu Arg Glu Ile Asn Lys Lys Ile Ala Ser Gly Glu Val Ser Ala Glu  
 1105 1110 1115 1120  
 Met Phe Cys Lys Phe Ser Ser Trp His Val Pro Ile Leu Ala Met Thr  
 1125 1130 1135  
 Ala Asp Val Ile Gln Ala Thr His Glu Glu Cys Met Lys Cys Gly Met  
 1140 1145 1150  
 Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Val Leu Tyr Thr Ala  
 1155 1160 1165  
 Val Ala Arg Phe Phe Glu Pro Cys  
 1170 1175

<210> 3

<211> 3111

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(3111)

&lt;400&gt; 3

atg agt ctg ttc cat gtg cta ggg ttt ggt gtc aag att ggg cat ctc	48
Met Ser Leu Phe His Val Leu Gly Phe Gly Val Lys Ile Gly His Leu	
1 5 10 15	
ttc tgg atg cta tgc tgc tgg ttt gtt tct tgg ttc gtt gat aat ggg	96
Phe Trp Met Leu Cys Cys Trp Phe Val Ser Trp Phe Val Asp Asn Gly	
20 25 30	
atc gag gac aag tct ggt ctt tta gtt ggc tct gtc ggt gat ctt gag	144
Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu	
35 40 45	
aag act aag atg act acg ttg aag aag aag aac aag atg tgg ttc tgg	192
Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp	
50 55 60	
aat aag atc tct agc agc gga ctc aag atc ccg agt ttc tct tat cag	240
Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln	
65 70 75 80	
ttt ctt ggc tct gtt aaa ttc aac aag gcg tgg tgg agg aag ctt gtg	288
Phe Leu Gly Ser Val Lys Phe Asn Lys Ala Trp Trp Arg Lys Leu Val	
85 90 95	
gtg gtt tgg gtt gtc ttc tgg gtc ttg gtc tct att tgg acg ttt tgg	336
Val Val Trp Val Val Phe Trp Val Leu Val Ser Ile Trp Thr Phe Trp	
100 105 110	
tac ttt agc tgc caa gct atg gag aag agg aaa gag acg cta gct agt	384
Tyr Phe Ser Ser Gln Ala Met Glu Lys Arg Lys Glu Thr Leu Ala Ser	
115 120 125	
atg tgt gat gag aga gct cgt atg ctg cag gat cag ttc aac gtt agc	432
Met Cys Asp Glu Arg Ala Arg Met Leu Gln Asp Gln Phe Asn Val Ser	
130 135 140	
atg aat cat gtt caa gcc atg tct atc ttg atc tca acc ttc cac cat	480
Met Asn His Val Gln Ala Met Ser Ile Leu Ile Ser Thr Phe His His	
145 150 155 160	
ggc aag att cct tct gct atc gat cag aga aca ttc tca gag tac act	528
Gly Lys Ile Pro Ser Ala Ile Asp Gln Arg Thr Phe Ser Glu Tyr Thr	
165 170 175	
gat aga act tcc ttt gag agg cct ctt act agc ggg gta gct tat gct	576
Asp Arg Thr Ser Phe Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala	
180 185 190	
atg agg gtg ctc cat tca gag agg gaa gag ttc gag agg caa caa ggt	624
Met Arg Val Leu His Ser Glu Arg Glu Glu Phe Glu Arg Gln Gln Gly	
195 200 205	
tgg act att agg aag atg tat tct ctt gaa caa aac cca gtt cac aag	672
Trp Thr Ile Arg Lys Met Tyr Ser Leu Glu Gln Asn Pro Val His Lys	
210 215 220	

gat gac tat gac ctg gaa gct ttg gaa cca tcc cct gtc caa gaa gag	720
Asp Asp Tyr Asp Leu Glu Ala Leu Glu Pro Ser Pro Val Gln Glu Glu	
225 230 235 240	
tac gct cca gtc atc ttt gct cag gac act gtt tct cac gtt gtt tct	768
Tyr Ala Pro Val Ile Phe Ala Gln Asp Thr Val Ser His Val Val Ser	
245 250 255	
ctc gat atg ctg tct ggg aaa gaa gat cgt gaa aac gtt ttg cgg gcc	816
Leu Asp Met Leu Ser Gly Lys Glu Asp Arg Glu Asn Val Leu Arg Ala	
260 265 270	
agg agt tca ggt aaa ggg gtt ttg aca gct cct ttc cca ttg ata aag	864
Arg Ser Ser Gly Lys Gly Val Leu Thr Ala Pro Phe Pro Leu Ile Lys	
275 280 285	
aca aat aga ctt ggg gtg atc ctg aca ttt gca gtg tac aag aga gat	912
Thr Asn Arg Leu Gly Val Ile Leu Thr Phe Ala Val Tyr Lys Arg Asp	
290 295 300	
ctc ccc tcc aat gca acg cca aaa gag aga att gag gct act aac ggg	960
Leu Pro Ser Asn Ala Thr Pro Lys Glu Arg Ile Glu Ala Thr Asn Gly	
305 310 315 320	
tat ctc ggg gga gtg ttt gac att gag tcc ctg gta gaa aac ttg ctt	1008
Tyr Leu Gly Gly Val Phe Asp Ile Glu Ser Leu Val Glu Asn Leu Leu	
325 330 335	
caa cag ctg gct agc aag caa acg att ctt gtc aat gtg tac gat atc	1056
Gln Gln Leu Ala Ser Lys Gln Thr Ile Leu Val Asn Val Tyr Asp Ile	
340 345 350	
acc aat cac tct caa ccg att agc atg tat ggt aca aat gtg tcg gct	1104
Thr Asn His Ser Gln Pro Ile Ser Met Tyr Gly Thr Asn Val Ser Ala	
355 360 365	
gat ggg ttg gaa cgt gtt agt cca cta atc ttt ggc gat cca ttg aga	1152
Asp Gly Leu Glu Arg Val Ser Pro Leu Ile Phe Gly Asp Pro Leu Arg	
370 375 380	
aag cat gag atg cgt tgc aga ttt aag cag aaa cca cca tgg cca gtg	1200
Lys His Glu Met Arg Cys Arg Phe Lys Gln Lys Pro Pro Trp Pro Val	
385 390 395 400	
cta tca atg gtg aca tca ttc ggt atc ctt gtg att gcg tta ctt gtt	1248
Leu Ser Met Val Thr Ser Phe Gly Ile Leu Val Ile Ala Leu Leu Val	
405 410 415	
gca cat ata atc cac gca acc gtt agt cga ata cac aaa gtt gaa gaa	1296
Ala His Ile Ile His Ala Thr Val Ser Arg Ile His Lys Val Glu Glu	
420 425 430	
gat tgt gat aaa atg aag cag ctc aag aaa aag gct gaa gca gca gat	1344
Asp Cys Asp Lys Met Lys Gln Leu Lys Lys Lys Ala Glu Ala Ala Asp	
435 440 445	

ggt gca aag tca cag ttc ctt gcc act gtt tca cat gaa atc aga act	1392
Val Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr	
450 455 460	
cca atg aat ggt gtt cta gga atg ttg cat atg ctt atg gac aca gag	1440
Pro Met Asn Gly Val Leu Gly Met Leu His Met Leu Met Asp Thr Glu	
465 470 475 480	
tta gat gtt acg caa cag gat tat gtt agg acc gca cag gca agt gga	1488
Leu Asp Val Thr Gln Gln Asp Tyr Val Arg Thr Ala Gln Ala Ser Gly	
485 490 495	
aaa gct tta gtc tcg cta ata aat gag gtt ttg gac caa gca aag att	1536
Lys Ala Leu Val Ser Leu Ile Asn Glu Val Leu Asp Gln Ala Lys Ile	
500 505 510	
gaa tct gga aag ctt gaa ctt gag gag gtg cgg ttt gat ttg aga gga	1584
Glu Ser Gly Lys Leu Glu Leu Glu Glu Val Arg Phe Asp Leu Arg Gly	
515 520 525	
ata tta gat gat gtc ctg tca ctc ttc tct agc aag tcc caa caa aag	1632
Ile Leu Asp Asp Val Leu Ser Leu Phe Ser Ser Lys Ser Gln Gln Lys	
530 535 540	
ggg gtg gag ttg gca gta tac ata tct gat cgt gtt cca gat atg tta	1680
Gly Val Glu Leu Ala Val Tyr Ile Ser Asp Arg Val Pro Asp Met Leu	
545 550 555 560	
att ggt gat cct ggg agg ttt cga caa ata ctc aca aat ctt atg ggt	1728
Ile Gly Asp Pro Gly Arg Phe Arg Gln Ile Leu Thr Asn Leu Met Gly	
565 570 575	
aat tcc att aag ttc act gag aaa gga cac atc ttt gta act gtt cat	1776
Asn Ser Ile Lys Phe Thr Glu Lys Gly His Ile Phe Val Thr Val His	
580 585 590	
ttg gtg gat gag cta ttt gaa tct atc gat gga gag aca gca tca tct	1824
Leu Val Asp Glu Leu Phe Glu Ser Ile Asp Gly Glu Thr Ala Ser Ser	
595 600 605	
ccg gaa agt aca ctg agt ggg ctt cca gtt gca gac cgg cag agg agc	1872
Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser	
610 615 620	
tgg gaa aac ttt aaa gct ttc agc tcc aac ggg cat cgg agc ttt gaa	1920
Trp Glu Asn Phe Lys Ala Phe Ser Ser Asn Gly His Arg Ser Phe Glu	
625 630 635 640	
cca tct ccc cct gat ata aac cta atc gtc tca gtt gag gat act ggc	1968
Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly	
645 650 655	
gta ggg atc cct gta gaa gcg cag tcc cgt att ttt acg cct ttc atg	2016
Val Gly Ile Pro Val Glu Ala Gln Ser Arg Ile Phe Thr Pro Phe Met	
660 665 670	

caa gtc gga cca tcc ata tcc agg acg cat gga ggc aca gga att gga	2064
Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly	
675 680 685	
ctt agc ata agc aaa tgt cta gtt gga ctg atg aag gga gaa att gga	2112
Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly	
690 695 700	
ttc tcg agt act ccc aag gtt ggg tcc aca ttc aca ttt act gct gta	2160
Phe Ser Ser Thr Pro Lys Val Gly Ser Thr Phe Thr Phe Thr Ala Val	
705 710 715 720	
ttt tcc aat ggg atg caa cca gct gaa aga aag aat gac aac aac cag	2208
Phe Ser Asn Gly Met Gln Pro Ala Glu Arg Lys Asn Asp Asn Asn Gln	
725 730 735	
ccc ata ttc tcg gaa ttc cgg ggc atg aaa gct gtg gtt gtg gac cat	2256
Pro Ile Phe Ser Glu Phe Arg Gly Met Lys Ala Val Val Val Asp His	
740 745 750	
agg cct gca agg gca aaa gtc tcg tgg tac cat ttt cag cgt ctt gga	2304
Arg Pro Ala Arg Ala Lys Val Ser Trp Tyr His Phe Gln Arg Leu Gly	
755 760 765	
att cga gtc gaa gta gtt cca cgt gtt gaa cag gct cta cat tat ctg	2352
Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu	
770 775 780	
aag att ggt act acc act gtg aat atg ata ctc ata gag caa gaa ata	2400
Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile	
785 790 795 800	
tgg aat agg gaa gca gat gat ttc att aaa aag cta cag aaa gac cct	2448
Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro	
805 810 815	
ctt ttc ctt tct cct aag ttg att ttg tta gca aac tca gta gaa tcg	2496
Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser	
820 825 830	
tca ata tca gag gct tta tgc acc ggt ata gat cct cca ata gtg ata	2544
Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile	
835 840 845	
gtg aaa cca ttg agg gcg agt atg cta gca gca act ttg cag agg gga	2592
Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly	
850 855 860	
ttg ggt att gga atc aga gaa cca cct caa cac aag gga cct cct gct	2640
Leu Gly Ile Gly Ile Arg Glu Pro Pro Gln His Lys Gly Pro Pro Ala	
865 870 875 880	
ttg att ctc agg aat ctt ctc ctt ggt aga aaa att tta atc gtg gat	2688
Leu Ile Leu Arg Asn Leu Leu Leu Gly Arg Lys Ile Leu Ile Val Asp	
885 890 895	

gat aac aac gta aac ctc aga gtg gca gcg gga gct ctg aaa aag tac 2736  
 Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr  
 900 905 910

gga gct gat gtg gtc tgc gct gag agt ggg ata aag gca atc tca ttg 2784  
 Gly Ala Asp Val Val Cys Ala Glu Ser Gly Ile Lys Ala Ile Ser Leu  
 915 920 925

ctt aag cca cct cac gag ttt gat gct tgc ttc atg gac att cag atg 2832  
 Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met  
 930 935 940

cca gaa atg gat gga ttt gaa gct aca agg aga ata cga gat atg gaa 2880  
 Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu  
 945 950 955 960

gag gag atg aac aag aga ata aag aat ggg gag gct ttg ata gta gag 2928  
 Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu  
 965 970 975

aac ggt aac aaa aca agc tgg cat ctt ccg gta tta gca atg acg gca 2976  
 Asn Gly Asn Lys Thr Ser Trp His Leu Pro Val Leu Ala Met Thr Ala  
 980 985 990

gat gtg atc caa gca acg cat gag gaa tgt ctg aag tgt gga atg gat 3024  
 Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp  
 995 1000 1005

ggg tat gta tca aaa cca ttt gaa gca gag cag ctg tac agg gaa gtt 3072  
 Gly Tyr Val Ser Lys Pro Phe Glu Ala Glu Gln Leu Tyr Arg Glu Val  
 1010 1015 1020

tct cgc ttt ttc aat tcg cct tca gat aca gaa tca taa 3111  
 Ser Arg Phe Phe Asn Ser Pro Ser Asp Thr Glu Ser  
 1025 1030 1035

&lt;210&gt; 4

&lt;211&gt; 1036

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 4

Met Ser Leu Phe His Val Leu Gly Phe Gly Val Lys Ile Gly His Leu  
1 5 10 15

Phe Trp Met Leu Cys Cys Trp Phe Val Ser Trp Phe Val Asp Asn Gly  
20 25 30

Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu  
35 40 45

Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp  
50 55 60

Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln  
65 70 75 80

Phe	Leu	Gly	Ser	Val	Lys	Phe	Asn	Lys	Ala	Trp	Trp	Arg	Lys	Leu	Val	85	90	95
Val	Val	Trp	Val	Val	Phe	Trp	Val	Leu	Val	Ser	Ile	Trp	Thr	Phe	Trp	100	105	110
Tyr	Phe	Ser	Ser	Gln	Ala	Met	Glu	Lys	Arg	Lys	Glu	Thr	Leu	Ala	Ser	115	120	125
Met	Cys	Asp	Glu	Arg	Ala	Arg	Met	Leu	Gln	Asp	Gln	Phe	Asn	Val	Ser	130	135	140
Met	Asn	His	Val	Gln	Ala	Met	Ser	Ile	Leu	Ile	Ser	Thr	Phe	His	His	145	150	155
Gly	Lys	Ile	Pro	Ser	Ala	Ile	Asp	Gln	Arg	Thr	Phe	Ser	Glu	Tyr	Thr	165	170	175
Asp	Arg	Thr	Ser	Phe	Glu	Arg	Pro	Leu	Thr	Ser	Gly	Val	Ala	Tyr	Ala	180	185	190
Met	Arg	Val	Leu	His	Ser	Glu	Arg	Glu	Glu	Phe	Glu	Arg	Gln	Gln	Gly	195	200	205
Trp	Thr	Ile	Arg	Lys	Met	Tyr	Ser	Leu	Glu	Gln	Asn	Pro	Val	His	Lys	210	215	220
Asp	Asp	Tyr	Asp	Leu	Glu	Ala	Leu	Glu	Pro	Ser	Pro	Val	Gln	Glu	Glu	225	230	235
Tyr	Ala	Pro	Val	Ile	Phe	Ala	Gln	Asp	Thr	Val	Ser	His	Val	Val	Ser	245	250	255
Leu	Asp	Met	Leu	Ser	Gly	Lys	Glu	Asp	Arg	Glu	Asn	Val	Leu	Arg	Ala	260	265	270
Arg	Ser	Ser	Gly	Lys	Gly	Val	Leu	Thr	Ala	Pro	Phe	Pro	Leu	Ile	Lys	275	280	285
Thr	Asn	Arg	Leu	Gly	Val	Ile	Leu	Thr	Phe	Ala	Val	Tyr	Lys	Arg	Asp	290	295	300
Leu	Pro	Ser	Asn	Ala	Thr	Pro	Lys	Glu	Arg	Ile	Glu	Ala	Thr	Asn	Gly	305	310	315
Tyr	Leu	Gly	Gly	Val	Phe	Asp	Ile	Glu	Ser	Leu	Val	Glu	Asn	Leu	Leu	325	330	335
Gln	Gln	Leu	Ala	Ser	Lys	Gln	Thr	Ile	Leu	Val	Asn	Val	Tyr	Asp	Ile	340	345	350
Thr	Asn	His	Ser	Gln	Pro	Ile	Ser	Met	Tyr	Gly	Thr	Asn	Val	Ser	Ala	355	360	365
Asp	Gly	Leu	Glu	Arg	Val	Ser	Pro	Leu	Ile	Phe	Gly	Asp	Pro	Leu	Arg	370	375	380



Lys His Glu Met Arg Cys Arg Phe Lys Gln Lys Pro Pro Trp Pro Val  
 385 390 395 400  
 Leu Ser Met Val Thr Ser Phe Gly Ile Leu Val Ile Ala Leu Leu Val  
 405 410 415  
 Ala His Ile Ile His Ala Thr Val Ser Arg Ile His Lys Val Glu Glu  
 420 425 430  
 Asp Cys Asp Lys Met Lys Gln Leu Lys Lys Lys Ala Glu Ala Ala Asp  
 435 440 445  
 Val Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr  
 450 455 460  
 Pro Met Asn Gly Val Leu Gly Met Leu His Met Leu Met Asp Thr Glu  
 465 470 475 480  
 Leu Asp Val Thr Gln Gln Asp Tyr Val Arg Thr Ala Gln Ala Ser Gly  
 485 490 495  
 Lys Ala Leu Val Ser Leu Ile Asn Glu Val Leu Asp Gln Ala Lys Ile  
 500 505 510  
 Glu Ser Gly Lys Leu Glu Leu Glu Glu Val Arg Phe Asp Leu Arg Gly  
 515 520 525  
 Ile Leu Asp Asp Val Leu Ser Leu Phe Ser Ser Lys Ser Gln Gln Lys  
 530 535 540  
 Gly Val Glu Leu Ala Val Tyr Ile Ser Asp Arg Val Pro Asp Met Leu  
 545 550 555 560  
 Ile Gly Asp Pro Gly Arg Phe Arg Gln Ile Leu Thr Asn Leu Met Gly  
 565 570 575  
 Asn Ser Ile Lys Phe Thr Glu Lys Gly His Ile Phe Val Thr Val His  
 580 585 590  
 Leu Val Asp Glu Leu Phe Glu Ser Ile Asp Gly Glu Thr Ala Ser Ser  
 595 600 605  
 Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser  
 610 615 620  
 Trp Glu Asn Phe Lys Ala Phe Ser Ser Asn Gly His Arg Ser Phe Glu  
 625 630 635 640  
 Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly  
 645 650 655  
 Val Gly Ile Pro Val Glu Ala Gln Ser Arg Ile Phe Thr Pro Phe Met  
 660 665 670  
 Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly  
 675 680 685

Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly  
 690 695 700  
 Phe Ser Ser Thr Pro Lys Val Gly Ser Thr Phe Thr Phe Thr Ala Val  
 705 710 715 720  
 Phe Ser Asn Gly Met Gln Pro Ala Glu Arg Lys Asn Asp Asn Asn Gln  
 725 730 735  
 Pro Ile Phe Ser Glu Phe Arg Gly Met Lys Ala Val Val Val Asp His  
 740 745 750  
 Arg Pro Ala Arg Ala Lys Val Ser Trp Tyr His Phe Gln Arg Leu Gly  
 755 760 765  
 Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu  
 770 775 780  
 Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile  
 785 790 795 800  
 Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro  
 805 810 815  
 Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser  
 820 825 830  
 Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile  
 835 840 845  
 Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly  
 850 855 860  
 Leu Gly Ile Gly Ile Arg Glu Pro Pro Gln His Lys Gly Pro Pro Ala  
 865 870 875 880  
 Leu Ile Leu Arg Asn Leu Leu Leu Gly Arg Lys Ile Leu Ile Val Asp  
 885 890 895  
 Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr  
 900 905 910  
 Gly Ala Asp Val Val Cys Ala Glu Ser Gly Ile Lys Ala Ile Ser Leu  
 915 920 925  
 Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met  
 930 935 940  
 Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu  
 945 950 955 960  
 Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu  
 965 970 975  
 Asn Gly Asn Lys Thr Ser Trp His Leu Pro Val Leu Ala Met Thr Ala  
 980 985 990

Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp  
 995 1000 1005

Gly Tyr Val Ser Lys Pro Phe Glu Ala Glu Gln Leu Tyr Arg Glu Val  
 1010 1015 1020

Ser Arg Phe Phe Asn Ser Pro Ser Asp Thr Glu Ser  
 1025 1030 1035

<210> 5

<211> 3174

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(3174)

<400> 5

atg aac tgg gca ctc aac aat cat caa gaa gaa gaa gaa gag cca cga 48  
 Met Asn Trp Ala Leu Asn Asn His Gln Glu Glu Glu Glu Glu Pro Arg  
 1 5 10 15

aga att gaa att tct gat tcc gag tca cta gaa aac ttg aaa agc agc 96  
 Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser  
 20 25 30

gat ttt tat caa ctg ggt ggt ggt ggt gct ctg aat tcg tca gaa aag 144  
 Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys  
 35 40 45

ccg aga aag atc gat ttt tgg cgt tcg ggg ttg atg ggt ttt gcg aag 192  
 Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys  
 50 55 60

atg cag cag cag caa cag ctt cag cat tca gtg gcg gtg aag atg aac 240  
 Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn  
 65 70 75 80

aat aat aat aat aac gat cta atg ggt aat aaa aaa ggg tca act ttc 288  
 Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe  
 85 90 95

ata caa gaa cat cga gca ttg tta cca aaa gct ttg att ctg tgg atc 336  
 Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile  
 100 105 110

atc att gtt ggg ttt ata agc agt ggg att tat cag tgg atg gat gat 384  
 Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp  
 115 120 125

gct aat aag att aga agg gaa gag gtt ttg gtc agc atg tgt gat caa 432  
 Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln  
 130 135 140

aga gct aga atg ttg cag gat caa ttt agt gtt agt gtt aat cat gtt	480
Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val	
145 150 155 160	
cat gct ttg gct att ctc gtc tcc act ttt cat tac cac aag aac cct	528
His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro	
165 170 175	
tct gca att gat cag gag aca ttt gcg gag tac acg gca aga aca gca	576
Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala	
180 185 190	
ttt gag aga ccg ttg cta agt gga gtg gct tat gct gaa aaa gtt gtg	624
Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val	
195 200 205	
aat ttt gag agg gag atg ttt gag cgg cag cac aat tgg gtt ata aag	672
Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys	
210 215 220	
aca atg gat aga gga gag cct tca ccg gtt agg gat gag tat gct cct	720
Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro	
225 230 235 240	
gtt ata ttc tct caa gat agt gtc tct tac ctt gag tca ctc gat atg	768
Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met	
245 250 255	
atg tca ggc gag gag gat cgt gag aat att ttg cga gct aga gaa acc	816
Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr	
260 265 270	
gga aaa gct gtc ttg act agc cct ttt agg ttg ttg gaa act cac cat	864
Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His	
275 280 285	
ctc gga gtt gtg ttg aca ttc cct gtc tac aag tct tct ctt cct gaa	912
Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu	
290 295 300	
aat ccg act gtc gaa gag cgt att gca gcc act gca ggg tac ctt ggt	960
Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly	
305 310 315 320	
ggt gcg ttt gat gtg gag tct cta gtc gag aat tta ctt ggt cag ctt	1008
Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu	
325 330 335	
gct ggt aac caa gca ata gtt gtg cat gtg tat gat atc acc aat gca	1056
Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala	
340 345 350	
tca gat cca ctt gtc atg tat ggt aat caa gat gaa gaa gcc gac aga	1104
Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg	
355 360 365	

tct	ctc	tct	cat	gag	agc	aag	ctc	gat	ttt	gga	gac	ccc	ttc	agg	aaa	1152
Ser	Leu	Ser	His	Glu	Ser	Lys	Leu	Asp	Phe	Gly	Asp	Pro	Phe	Arg	Lys	
370						375					380					
cat	aag	atg	ata	tgc	agg	tac	cac	caa	aag	gca	cca	ata	cca	ttg	aat	1200
His	Lys	Met	Ile	Cys	Arg	Tyr	His	Gln	Lys	Ala	Pro	Ile	Pro	Leu	Asn	
385					390					395					400	
gtg	ctc	aca	act	gtg	cca	ttg	ttc	ttt	gcg	att	ggg	ttc	ttg	gtg	ggg	1248
Val	Leu	Thr	Thr	Val	Pro	Leu	Phe	Phe	Ala	Ile	Gly	Phe	Leu	Val	Gly	
				405					410					415		
tat	ata	ctg	tat	ggg	gca	gct	atg	cac	ata	gta	aaa	gtc	gaa	gat	gat	1296
Tyr	Ile	Leu	Tyr	Gly	Ala	Ala	Met	His	Ile	Val	Lys	Val	Glu	Asp	Asp	
			420					425					430			
ttc	cat	gaa	atg	caa	gag	ctt	aaa	gtg	cga	gca	gaa	gct	gct	gat	gtc	1344
Phe	His	Glu	Met	Gln	Glu	Leu	Lys	Val	Arg	Ala	Glu	Ala	Ala	Asp	Val	
		435					440					445				
gct	aaa	tcg	cag	ttt	ctt	gct	acc	gtg	tct	cac	gag	atc	agg	aca	cca	1392
Ala	Lys	Ser	Gln	Phe	Leu	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro	
	450					455					460					
atg	aat	ggc	att	ctc	gga	atg	ctt	gct	atg	ctc	cta	gat	aca	gaa	cta	1440
Met	Asn	Gly	Ile	Leu	Gly	Met	Leu	Ala	Met	Leu	Leu	Asp	Thr	Glu	Leu	
465					470					475					480	
agc	tcg	aca	cag	aga	gat	tac	gct	caa	acc	gct	caa	gta	tgt	ggg	aaa	1488
Ser	Ser	Thr	Gln	Arg	Asp	Tyr	Ala	Gln	Thr	Ala	Gln	Val	Cys	Gly	Lys	
				485					490					495		
gct	ttg	att	gca	ttg	ata	aat	gag	gtt	ctt	gat	cgc	gcc	aag	att	gaa	1536
Ala	Leu	Ile	Ala	Leu	Ile	Asn	Glu	Val	Leu	Asp	Arg	Ala	Lys	Ile	Glu	
			500					505					510			
gct	gga	aag	ctg	gag	ttg	gaa	tca	gta	cca	ttt	gat	atc	cgt	tca	ata	1584
Ala	Gly	Lys	Leu	Glu	Leu	Glu	Ser	Val	Pro	Phe	Asp	Ile	Arg	Ser	Ile	
		515					520					525				
ttg	gat	gat	gtc	ctt	tct	cta	ttc	tct	gag	gag	tca	agg	aac	aaa	ggc	1632
Leu	Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Glu	Glu	Ser	Arg	Asn	Lys	Gly	
	530					535					540					
att	gag	ctc	gcg	gtt	ttc	gtt	tca	gac	aaa	gta	cca	gag	ata	gtc	aaa	1680
Ile	Glu	Leu	Ala	Val	Phe	Val	Ser	Asp	Lys	Val	Pro	Glu	Ile	Val	Lys	
545					550					555					560	
gga	gat	tca	ggg	aga	ttt	aga	cag	ata	atc	ata	aac	ctt	gtt	gga	aat	1728
Gly	Asp	Ser	Gly	Arg	Phe	Arg	Gln	Ile	Ile	Ile	Asn	Leu	Val	Gly	Asn	
				565					570					575		
tcg	gtt	aaa	ttc	aca	gag	aaa	gga	cat	atc	ttt	gtt	aaa	gtc	cat	ctt	1776
Ser	Val	Lys	Phe	Thr	Glu	Lys	Gly	His	Ile	Phe	Val	Lys	Val	His	Leu	
			580					585					590			

gcg gaa caa tca aaa gat gaa tct gaa ccg aaa aat gca ttg aat ggt	1824
Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly	
595 600 605	
gga gtg tct gaa gaa atg atc gtt gtt tcc aaa cag tca agt tac aac	1872
Gly Val Ser Glu Glu Met Ile Val Val Ser Lys Gln Ser Ser Tyr Asn	
610 615 620	
aca ttg agc ggt tac gaa gct gct gat ggt cgg aat agc tgg gat tca	1920
Thr Leu Ser Gly Tyr Glu Ala Ala Asp Gly Arg Asn Ser Trp Asp Ser	
625 630 635 640	
ttc aag cat ttg gtc tct gag gag cag tca tta tcg gag ttt gat att	1968
Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile	
645 650 655	
tct agc aat gtt agg ctt atg gtt tca atc gaa gac acg ggt att gga	2016
Ser Ser Asn Val Arg Leu Met Val Ser Ile Glu Asp Thr Gly Ile Gly	
660 665 670	
atc cct tta gtt gca caa ggc cgt gtg ttt atg ccg ttt atg caa gca	2064
Ile Pro Leu Val Ala Gln Gly Arg Val Phe Met Pro Phe Met Gln Ala	
675 680 685	
gat agc tcg act tca aga aac tat gga ggt act ggt att ggt ttg agt	2112
Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser	
690 695 700	
ata agc aag tgt ctt gtt gaa ctt atg cgt ggt cag ata aat ttc ata	2160
Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile	
705 710 715 720	
agc cgg cct cat att gga agc acg ttc tgg ttc acg gct gtt tta gag	2208
Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu	
725 730 735	
aaa tgc gat aaa tgc agt gcg att aac cat atg aag aaa cct aat gtg	2256
Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val	
740 745 750	
gaa cac ttg cct tct act ttt aaa gga atg aaa gct ata gtt gtt gat	2304
Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp	
755 760 765	
gct aag cct gtt aga gct gct gtg act aga tac cat atg aaa aga ctc	2352
Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu	
770 775 780	
gga atc aat gtt gat gtc gtg aca agt ctc aaa acc gct gtt gtt gca	2400
Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala	
785 790 795 800	
gct gct gcg ttt gaa aga aac ggt tct cct ctc cca aca aaa ccg caa	2448
Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln	
805 810 815	

ctt gat atg atc tta gta gag aaa gat tca tgg att tca act gaa gat	2496
Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp	
820 825 830	
aat gac tca gag att cgt tta ttg aat tca aga acc aac gga aac gtt	2544
Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val	
835 840 845	
cat cac aag tct ccg aaa cta gct cta ttc gca aca aac atc aca aat	2592
His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn	
850 855 860	
tcg gag ttc gac aga gct aaa tcc gca gga ttt gca gat acg gta ata	2640
Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile	
865 870 875 880	
atg aaa ccg tta aga gca agc atg att ggg gcg tgt ctg caa caa gtt	2688
Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val	
885 890 895	
ctc gag ctg aga aaa aca aga caa caa cat cca gaa gga tca tca ccc	2736
Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro	
900 905 910	
gca act ctc aag agc ttg ctt aca ggg aag aag att ctt gtg gtt gat	2784
Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp	
915 920 925	
gat aat ata gtt aac agg aga gta gct gca gga gct ctc aag aaa ttt	2832
Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe	
930 935 940	
gga gca gaa gtg gtt tgt gca gag agt ggt caa gtt gct ttg ggt ttg	2880
Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu	
945 950 955 960	
ctt cag att cca cac act ttc gat gct tgc ttc atg gat att caa atg	2928
Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met	
965 970 975	
cca cag atg gac gga ttt gaa gca act cgt cag ata aga atg atg gag	2976
Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu	
980 985 990	
aag gaa gct aaa gag aag acg aat ctc gaa tgg cat tta ccg att cta	3024
Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu	
995 1000 1005	
gcg atg act gcg gat gtg ata cac gcg acc tac gag gaa tgt ctg aaa	3072
Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys	
1010 1015 1020	
agt ggg atg gat ggt tac gtc tcc aaa cct ttt gaa gaa gag aat ctc	3120
Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu	
1025 1030 1035 1040	

tat aaa tcc gtt gcc aaa tca ttc aaa cct aat cct atc tca cct tcg 3168  
 Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser  
                   1045                  1050                  1055

tcg taa 3174  
 Ser

<210> 6

<211> 1057

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met Asn Trp Ala Leu Asn Asn His Gln Glu Glu Glu Glu Glu Pro Arg  
   1                  5                  10                  15

Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser  
                   20                  25                  30

Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys  
                   35                  40                  45

Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys  
                   50                  55                  60

Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn  
   65                  70                  75                  80

Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe  
                   85                  90                  95

Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile  
                   100                  105                  110

Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp  
                   115                  120                  125

Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln  
                   130                  135                  140

Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val  
   145                  150                  155                  160

His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro  
                   165                  170                  175

Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala  
                   180                  185                  190

Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val  
                   195                  200                  205

Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys  
                   210                  215                  220

Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro  
   225                  230                  235                  240



Val	Ile	Phe	Ser	Gln	Asp	Ser	Val	Ser	Tyr	Leu	Glu	Ser	Leu	Asp	Met	245	250	255
Met	Ser	Gly	Glu	Glu	Asp	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Arg	Glu	Thr	260	265	270
Gly	Lys	Ala	Val	Leu	Thr	Ser	Pro	Phe	Arg	Leu	Leu	Glu	Thr	His	His	275	280	285
Leu	Gly	Val	Val	Leu	Thr	Phe	Pro	Val	Tyr	Lys	Ser	Ser	Leu	Pro	Glu	290	295	300
Asn	Pro	Thr	Val	Glu	Glu	Arg	Ile	Ala	Ala	Thr	Ala	Gly	Tyr	Leu	Gly	305	310	315
Gly	Ala	Phe	Asp	Val	Glu	Ser	Leu	Val	Glu	Asn	Leu	Leu	Gly	Gln	Leu	325	330	335
Ala	Gly	Asn	Gln	Ala	Ile	Val	Val	His	Val	Tyr	Asp	Ile	Thr	Asn	Ala	340	345	350
Ser	Asp	Pro	Leu	Val	Met	Tyr	Gly	Asn	Gln	Asp	Glu	Glu	Ala	Asp	Arg	355	360	365
Ser	Leu	Ser	His	Glu	Ser	Lys	Leu	Asp	Phe	Gly	Asp	Pro	Phe	Arg	Lys	370	375	380
His	Lys	Met	Ile	Cys	Arg	Tyr	His	Gln	Lys	Ala	Pro	Ile	Pro	Leu	Asn	385	390	395
Val	Leu	Thr	Thr	Val	Pro	Leu	Phe	Phe	Ala	Ile	Gly	Phe	Leu	Val	Gly	405	410	415
Tyr	Ile	Leu	Tyr	Gly	Ala	Ala	Met	His	Ile	Val	Lys	Val	Glu	Asp	Asp	420	425	430
Phe	His	Glu	Met	Gln	Glu	Leu	Lys	Val	Arg	Ala	Glu	Ala	Ala	Asp	Val	435	440	445
Ala	Lys	Ser	Gln	Phe	Leu	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro	450	455	460
Met	Asn	Gly	Ile	Leu	Gly	Met	Leu	Ala	Met	Leu	Leu	Asp	Thr	Glu	Leu	465	470	475
Ser	Ser	Thr	Gln	Arg	Asp	Tyr	Ala	Gln	Thr	Ala	Gln	Val	Cys	Gly	Lys	485	490	495
Ala	Leu	Ile	Ala	Leu	Ile	Asn	Glu	Val	Leu	Asp	Arg	Ala	Lys	Ile	Glu	500	505	510
Ala	Gly	Lys	Leu	Glu	Leu	Glu	Ser	Val	Pro	Phe	Asp	Ile	Arg	Ser	Ile	515	520	525
Leu	Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Glu	Glu	Ser	Arg	Asn	Lys	Gly	530	535	540

Ile Glu Leu Ala Val Phe Val Ser Asp Lys Val Pro Glu Ile Val Lys  
 545 550 555 560  
 Gly Asp Ser Gly Arg Phe Arg Gln Ile Ile Ile Asn Leu Val Gly Asn  
 565 570 575  
 Ser Val Lys Phe Thr Glu Lys Gly His Ile Phe Val Lys Val His Leu  
 580 585 590  
 Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly  
 595 600 605  
 Gly Val Ser Glu Glu Met Ile Val Val Ser Lys Gln Ser Ser Tyr Asn  
 610 615 620  
 Thr Leu Ser Gly Tyr Glu Ala Ala Asp Gly Arg Asn Ser Trp Asp Ser  
 625 630 635 640  
 Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile  
 645 650 655  
 Ser Ser Asn Val Arg Leu Met Val Ser Ile Glu Asp Thr Gly Ile Gly  
 660 665 670  
 Ile Pro Leu Val Ala Gln Gly Arg Val Phe Met Pro Phe Met Gln Ala  
 675 680 685  
 Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser  
 690 695 700  
 Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile  
 705 710 715 720  
 Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu  
 725 730 735  
 Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val  
 740 745 750  
 Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp  
 755 760 765  
 Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu  
 770 775 780  
 Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala  
 785 790 795 800  
 Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln  
 805 810 815  
 Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp  
 820 825 830  
 Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val  
 835 840 845

His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn  
 850 855 860  
 Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile  
 865 870 875 880  
 Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val  
 885 890 895  
 Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro  
 900 905 910  
 Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp  
 915 920 925  
 Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe  
 930 935 940  
 Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu  
 945 950 955 960  
 Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met  
 965 970 975  
 Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu  
 980 985 990  
 Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu  
 995 1000 1005  
 Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys  
 1010 1015 1020  
 Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu  
 1025 1030 1035 1040  
 Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser  
 1045 1050 1055

Ser

<210> 7  
 <211> 125  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 7  
 Glu Thr Ser Val Lys Ile Leu Val Val Glu Asp Asn His Val Asn Gln  
 1 5 10 15  
 Glu Val Ile Lys Arg Met Leu Asn Leu Glu Gly Ile Glu Asn Ile Glu  
 20 25 30  
 Leu Ala Cys Asp Gly Gln Glu Ala Phe Asp Lys Val Lys Glu Leu Thr  
 35 40 45

Ser Lys Gly Glu Asn Tyr Asn Met Ile Phe Met Asp Val Gln Met Pro  
 50 55 60

Lys Val Asp Gly Leu Leu Ser Thr Lys Met Ile Arg Arg Asp Leu Gly  
 65 70 75 80

Tyr Thr Ser Pro Ile Val Ala Leu Thr Ala Phe Ala Asp Asp Ser Asn  
 85 90 95

Ile Lys Glu Cys Leu Glu Ser Gly Met Asn Gly Phe Leu Ser Lys Pro  
 100 105 110

Ile Lys Arg Pro Lys Leu Lys Thr Ile Leu Thr Glu Phe  
 115 120 125

<210> 8  
 <211> 118  
 <212> PRT  
 <213> Escherichia coli

<400> 8  
 Asn Asp Asp Met Met Ile Leu Val Val Asp Asp His Pro Ile Asn Arg  
 1 5 10 15

Arg Leu Leu Ala Asp Gln Leu Gly Ser Leu Gly Tyr Gln Cys Lys Thr  
 20 25 30

Ala Asn Asp Gly Val Asp Ala Leu Asn Val Leu Ser Lys Asn His Ile  
 35 40 45

Asp Ile Val Leu Ser Asp Val Asn Met Pro Asn Met Asp Gly Tyr Arg  
 50 55 60

Leu Thr Gln Arg Ile Arg Gln Leu Gly Leu Thr Leu Pro Val Ile Gly  
 65 70 75 80

Val Thr Ala Asn Ala Leu Ala Glu Glu Lys Gln Arg Cys Leu Glu Ser  
 85 90 95

Gly Met Asp Ser Cys Leu Ser Lys Pro Val Thr Leu Asp Val Ile Lys  
 100 105 110

Gln Ser Leu Thr Leu Tyr  
 115

<210> 9  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide primer for PCR

<400> 9  
 tccccgcgga aaatgttctt acggttaggt ag

<210> 10  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 10  
tcggtcgact tatgattctg tatctgaagg cga 33

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 11  
tcagatatga actgggcact caac 24

<210> 12  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 12  
ctcaatgctt ttgttccttg actc 24

<210> 13  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 13  
accatgaact gggcactcaa caatcatcaa g 31

<210> 14  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 14

ggattacgac gaaggtgaga taggattagg

30

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 15

gatccagct agctagggcc ctaccgcggg ga

32

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 16

tccccgcgga aaatgttctt acggttaggt ag

32

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 17

tcggtcgact tatgattctg tatctgaagg cga

33

<210> 18

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 18  
ctagtccccg cggtagggcc ctagctagct gg 32

<210> 19  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 19  
tccccgcgga aaatgtctat aacttgtag c 31

<210> 20  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 20  
ctagctagct taacaagggtt caaagaatct tgc 33

<210> 21  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 21  
tccccgcgga aaatgaaagc acgaggtag agg 33

<210> 22  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide primer for PCR

<400> 22  
ctagctagct taacaagggtt caaagaattt gc 32